

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 28, 2002, 17:31:09 ; Search time 63.43 Seconds
(without alignments)
613.651 Million cell updates/sec

Title: US-09-502-984B-1
Perfect score: 1194
Sequence: 1 APPPNLPDPKFEKKAALAA.....GGFWSAMSEPSILTPSDLD 225

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1005.5	84.2	509	6 Q9MYZ9	Q9MYZ9 sus scrofa
2	965.5	80.9	316	11 O35545	O35545 rattus norv
3	851	71.3	229	6 Q27950	Q27950 bos indicus
4	846	70.9	229	6 Q28206	Q28206 bos taurus
5	778.5	65.2	387	6 Q95N13	Q95N13 ovis aries
6	778.5	65.2	418	6 Q95N14	Q95N14 ovis aries
7	185	15.5	566	11 Q925F5	Q925F5 mus musculu
8	160.5	13.4	422	4 Q75462	Q75462 homo sapien
9	159.5	13.4	422	4 Q9UHH5	Q9UHH5 homo sapien
10	159	13.3	296	6 O18880	O18880 bos taurus
11	157.5	13.2	425	11 Q9JMS8	Q9JMS8 mus musculu
12	151	12.6	581	6 O45561	O45561 ovis aries
13	140.5	11.8	626	13 Q90WG7	Q90WG7 cynops pyrr
14	140	11.7	227	6 Q9GLM3	Q9GLM3 ursus marit
15	139	11.6	625	6 Q9XS92	Q9XS92 trichosurus
16	137	11.5	622	6 Q9N0J7	Q9N0J7 callithrix

ALIGNMENTS

17	128	10.7	288	4 Q96P36	Q96P36 homo sapien
18	128	10.7	349	4 Q9UHU5	Q9UHU5 homo sapien
19	128	10.7	376	4 Q96P35	Q96P35 homo sapien
20	126	10.6	521	4 Q96TF0	Q96TF0 homo sapien
21	126	10.6	608	11 Q99JZ1	Q99JZ1 mus musculu
22	124.5	10.4	611	13 Q9PTI9	Q9PTI9 xenopus lae
23	123.5	10.3	636	13 Q90Z16	Q90Z16 parallithy
24	123.5	10.3	1093	11 Q70535	Q70535 rattus norv
25	122.5	10.3	634	6 Q46600	Q46600 bos taurus
26	122	10.2	206	4 Q16354	Q16354 homo sapien
27	122	10.2	346	13 Q93404	Q93404 oreochromis
28	120.5	10.1	638	6 Q95JF2	Q95JF2 alluropoda
29	118.5	9.9	538	13 Q9DFU0	Q9DFU0 sparus aura
30	114.5	9.6	608	6 Q9N0Y7	Q9N0Y7 monodelphis
31	113.5	9.5	4280	5 Q9UBZ9	Q9UBZ9 caenorhabdi
32	113.5	9.5	4450	5 Q9UBZ8	Q9UBZ8 caenorhabdi
33	112.5	9.4	638	6 Q9TU69	Q9TU69 canis famli
34	111.5	9.3	611	13 Q91BF6	Q91BF6 xenopus lae
35	111.5	9.3	611	13 Q9PTI0	Q9PTI0 xenopus lae
36	111	9.3	198	6 Q18985	Q18985 cervus elap
37	110.5	9.3	632	6 Q95ML5	Q95ML5 salmatri bol
38	109	9.1	600	13 Q9PTP0	Q9PTP0 carassius a
39	108.5	9.1	467	11 Q63216	Q63216 rattus norv
40	107.5	9.0	615	13 Q9DB35	Q9DB35 pelodiscus
41	107.5	9.0	628	11 Q9JKT1	Q9JKT1 cavia porce
42	107.5	9.0	628	11 Q9JKT1	Q9JKT1 cavia porce
43	107.5	9.0	628	11 Q9J197	Q9J197 cavia porce
44	106.5	8.9	229	4 Q14213	Q14213 homo sapien
45	106.5	8.9	390	4 Q9UEH7	Q9UEH7 homo sapien

RESULT 1
Q9MYZ9 PRELIMINARY; PRT; 509 AA.
AC Q9MYZ9;
ID 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ERYTHROPOIETIN RECEPTOR.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Pearson P.L., Smith T.P.L., Sonstegard T.S., Klemcke H.G.,
Christenson R.K., Vallet J.L.;
RT "Porcine Erythropoietin Receptor: Molecular Cloning and Expression in
Embryonic and Fetal Liver."
RT Domest. Anim. Endocrinol. 0:0-0(2000).
DR EMBL; AF274305; AAF77065.1; -.
DR HSSP; P19235; 1BBA.
DR InterPro: IPR002996; CRIA.
DR InterPro: IPR000572; Euk_oxidored_molyb.
DR InterPro: IPR003861; FN_III.
DR InterPro: IPR003528; Hematopo_receptor_L_F1.
DR Pfam; PF00041; fn3; 1.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
DR PROSITE; PS00559; MOLYBDOPTERIN_EUK; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 509 AA; 55183 MW; 35B565D07C6BCDBA CRC64;

Query Match 84.2%; Score 1005.5; DB 6; Length 509;
Best Local Similarity 84.5%; Pred. No. 1.6e-86;
Matches 191; Conservative 9; Mismatches 25; Indels 1; Gaps 1;
QY 1 APPPNLPDPKFEKKAALAAKGPEELLCFTRELDLVCFWEAASAGVGPNYSFYLE 60

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DB 25 APSNPDAFESKAAALAAARGPEELCTFEREDLVCFWEAGSAGVPEDEYSFSTOLE 84
QY 61 DEPMKLCRLHOAPFARGAVFMCSLPTADTSSVPLELRT-AASGAPRHVRIHINEV 119
DB 85 GEFMKRCHLHOGTARGSVFMCSLPTADTSSVPLELRTVEYSSGAPRHRIHINEV 144
QY 120 LDAPVGLVARLADESGHVLRMLPPETPMTSHIRYEVDSAGNGASVQRYVEILEGRT 179
DB 145 LDPPAGLLARAEESGHVLRMLPPGAPMASLIRYEVNISTENAGGVQRYVEILDGRT 204
QY 180 ECVLSNLRGRTYTFVAVRAMAEPSCGFGFMSAMSEPSVLTTPSDLD 225
DB 205 ECVLSNLRGRTYTFVAVRAMAEPSCGFGFMSAMSEPSVLTTPSDLD 250

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RESULT 2
ID 035545 PRELIMINARY; PRT: 316 AA.
AC 035545;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE INTERON 5-INSERTED FORM OF ERYTHROPOIETIN RECEPTOR PRECURSOR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9829611; PubMed=9630610;
RA Yamaï R., Murakami C., Takenoshita M., Tsuyama S., Inui H.,
RA Miyatake K., Nakano Y.;
RT "The intron 5-inserted form of rat erythropoietin receptor is
RT expressed as a membrane-bound form."
RL Biochim. Biophys. Acta 1403:169-178(1998).
DR EMBL: D83509; BAA22373.1; -.
DR HSSP: P19235; IEBA.
DR InterPro: IPR002996; CRIA.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003528; Hematopo_receptor_L_F1.
DR Pfam: PF00041; fn3; 1.
DR SMART: SM00060; FN3; 1.
DR PROSITE: PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
KW Signal; Receptor.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 316 POTENTIAL.
SQ SEQUENCE 316 AA; 34220 MW; 05C44BF8516C180B CRC64;

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Query Match 80.9%; Score 965.5; DB 11; Length 316;
 Best Local Similarity 82.4%; Pred. No. 5.2e-83;
 Matches 183; Conservative 15; Mismatches 23; Indels 1; Gaps 1;

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QY 1 APPPNLPDPFESKAAALAAARGPEELCTFEREDLVCFWEBAASAGVGCNTSFSQLE 60
DB 25 ASSPSLPDPFESKAAALAAARGPEELCTFEREDLVCFWEBAASAGVGCNTSFSQLE 83
QY 61 DEPMKLCRLHOAPFARGAVFMCSLPTADTSSVPLELRTVTAAGAPRHVRIHINEV 120
DB 84 GESRKSCRLHOAPFARGAVFMCSLPTADTSSVPLELRTVTAAGAPRHVRIHINEV 143
QY 121 LDAPVGLVARLADESGHVLRMLPPETPMTSHIRYEVDSAGNGASVQRYVEILEGRT 180
DB 144 LDAPVGLVARLADESGHVLRMLPPETPMTSHIRYEVDSAGNGASVQRYVEILEGRT 203
QY 181 ECVLSNLRGRTYTFVAVRAMAEPSCGFGFMSAMSEPSVLTTPS 222
DB 204 ECVLSNLRGRTYTFVAVRAMAEPSCGFGFMSAMSEPSVLTTPS 245

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RESULT 3
 Q27950

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ID 027950 PRELIMINARY; PRT: 229 AA.
AC 027950;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ERYTHROPOIETIN RECEPTOR (FRAGMENT).
GN EFOR.
OS Bos indicus (Zebu).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BONE MARROW;
RA Sullivan H.B., Feldman B.F., Majiwa P.A.O., Logan-Henfrey L.L.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U61398; AAB03870.1; -.
DR HSSP: P19235; IEBA.
DR InterPro: IPR002996; CRIA.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003528; Hematopo_receptor_L_F1.
DR Pfam: PF00041; fn3; 1.
DR SMART: SM00060; FN3; 1.
DR PROSITE: PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 229 229
SQ SEQUENCE 229 AA; 25196 MW; F6E01CAAB07893E8 CRC64;

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Query Match 71.3%; Score 851; DB 6; Length 229;
 Best Local Similarity 84.3%; Pred. No. 2.2e-72;
 Matches 161; Conservative 6; Mismatches 24; Indels 0; Gaps 0;

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QY 35 DLVCFWEBAASAGVGCNTSFSQLEDEPMKLCRLHOAPFARGAVFMCSLPTADTSSFY 94
DB 1 DLVCFWEBAATAGVGCNTSFSQLEDEPMKLCRLHOAPFARGAVFMCSLPTADTSSFY 60
QY 95 PLELHYTAASGAPRHVRIHINEVLDAPVGLVARLADESGHVLRMLPPETPMTSHI 154
DB 61 PLELHYTAASGAPRHVRIHINEVLDAPVGLVARLADESGHVLRMLPPETPMTSHI 120
QY 155 RYEVDSAGNGASVQRYVEILEGRTVEYSSGAPRHRIHINEV 214
DB 121 RYEVNISAENNAASAOBYVEILDGRTVEYSSGAPRHRIHINEV 180
QY 215 PVSLLTPSDLD 225
DB 181 PASLLTPSDLD 191

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RESULT 4
ID 028206 PRELIMINARY; PRT: 229 AA.
AC 028206;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ERYTHROPOIETIN RECEPTOR (FRAGMENT).
GN EFOR.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BONE MARROW;
RA Sullivan H.B., Feldman B.F., Majiwa P.A.O., Logan-Henfrey L.L.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U61399; AAB03871.1; -.
DR HSSP: P19235; IEBA.

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SEQUENCE 566 AA; 63339 MW; A19D3DD5F7BDBA6B CRC64;

Query Match 15.5%; Score 185; DB 11; Length 566;

Best Local Similarity 27.0%; Pred. No. 4.1e-09; Mismatches 100; Indels 42; Gaps 7;

13 SKAALLAARGPEELLCFTERTEDLVCFWEBAASAGVPGNYSFYOLEDEPMKLCRLHQA 72

18 SQDFLLALGTETPLNCFQTFEDLTCFWEDEEAA--PSGYQLLYAVRGKPRACPLYSQ 75

73 PARGAVREMCSPPTAD-TSSFVPLELRYTAAS-GAPRIHRYIHT-----NE 117

76 SVPTFGTRYVQCPADDEVLFEPFLHMKVNSLNOTLLORLFVDSVETCCPTLMMPNP 135

118 VVLLDAPVGVVARLADSGHVLRWLPPPETMTHSHRYVDVSAGAGSVORVELLEG 177

136 VPLDPPCPVHPPTASQPHGV--RTSPAGAPF-----LTKGGS----- 173

178 RTECVLSNLGRTRYTFVAVRARMAPSPFGGFWASMESEPSLLTPSD 223

174 ---CIVSGIQAGKSYMLQLRSPDGVSLRSGMSPSPVVDLPD 216

RESULT 8 PRELIMINARY; PRT; 422 AA.

ID 075462 PRELIMINARY; PRT; 422 AA.

AC 075462; PRELIMINARY; PRT; 422 AA.

DT 01-NOV-1998 (TREMBLrel. 08, Created)

DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE CYTOKINE-LIKE FACTOR-1 PRECURSOR.

GN CLF-1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCB1_TaxID=9606;

RP SEQUENCE FROM N.A.

RA Elson G.C.A., Graber P., Losberger P., Herren S., Gretener D.,

RA Menoud L.N., Wells T.N.C., Kosco-Villbols M.H., Gauchat J.F.;

RT CLF-1, a Novel Soluble Protein Shares Homology with Members of the

RT Cytokine Type-1 Receptor Family.;

RL J. Immunol. 0:0-0(1998).

RP SEQUENCE FROM N.A.

RA Magrangeas F., Jacques Y., Minvielle S.;

RT Cloning and expression of a novel soluble protein containing

RT hematopoietic cytokine receptor domains.;

RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF059293; AAC28335.1; -

DR HSSP: P16471; 1BP3.

DR InterPro: IPR002996; CRIA.

DR InterPro: IPR003961; FN_III.

DR Pfam: PFO041; fn3; 2.

DR SMART: SM00060; FN3; 2.

KW Signal; Receptor.

FT SIGNAL 1 37

FT CHAIN 38 422

FT SEQUENCE 422 AA; 46301 MW; AD9DFCB01B84228 CRC64;

Query Match 13.4%; Score 160.5; DB 4; Length 422;

Best Local Similarity 26.3%; Pred. No. 5.8e-07; Mismatches 84; Indels 55; Gaps 13;

23 PEBLLCFTERTEDLVCFWEBAASAGVPG-----NYSFSYOLEDEPW---KLCRL 69

138 PVAISCSMKMKDLTCWT-----PGAHGFTPLHTNLSLKYLKLR---WYGQDNICEE 186

70 HQAPTRARGAVRFMCSPPTADTSSFVPLELRYTAAS--GAPRIH-RVIHINEVLLDAPVG 126

187 YHTVGPHS-----CHIP-KDLALFTPEIWEATNRLSARSQDVLTLIDLVTYTTDPPD 240

127 L-VARLADESGHYVLRWLPPPET-----PMTSHIREYVDVSAGNGAGSVORVELLEGRT 180

241 VHSRKGLEDDQLSVRWSPFPALKDFLFOAKYQIRIRVEDSV-----DKKVVDDVSNQIS 295

181 CVLSNLGRTRYTFVAVRARMAPSPFG-----GFWASMESEPSLLTP 221

296 CRLAGLKPGTVFVQVRCN----PFGYGSKKAGIWEWSHPTAATSP 339

RESULT 9 PRELIMINARY; PRT; 422 AA.

ID 090H5 PRELIMINARY; PRT; 422 AA.

AC 090H5; PRELIMINARY; PRT; 422 AA.

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE CLASS I CYTOKINE RECEPTOR.

GN ZCYTOR5.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCB1_TaxID=9606;

RP SEQUENCE FROM N.A.

RA Lok S., Presnell S.R., Jelmberg A.C., Gilbert T., Whitmore T.E.,

RA Foster D.C., Adams R.L., Lehner J.M., O'Hara P.J.;

RT Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF178684; AAD54385.1; -

DR HSSP: P16471; 1BP3.

DR InterPro: IPR002996; CRIA.

DR InterPro: IPR003961; FN_III.

DR Pfam: PFO0041; fn3; 2.

DR SMART: SM00060; FN3; 2.

KW Receptor.

FT SIGNAL 1 37

FT CHAIN 38 422

FT SEQUENCE 422 AA; 46315 MW; 0D2C5F7A01B942EE CRC64;

Query Match 13.4%; Score 159.5; DB 4; Length 422;

Best Local Similarity 26.3%; Pred. No. 7.3e-07; Mismatches 84; Indels 55; Gaps 13;

23 PEBLLCFTERTEDLVCFWEBAASAGVPG-----NYSFSYOLEDEPW---KLCRL 69

138 PVAISCSMKMKDLTCWT-----PGAHGFTPLHTNLSLKYLKLR---WYGQDNICEE 186

70 HQAPTRARGAVRFMCSPPTADTSSFVPLELRYTAAS--GAPRIH-RVIHINEVLLDAPVG 126

187 YHTVGPHS-----CHIP-KDLALFTPEIWEATNRLSARSQDVLTLIDLVTYTTDPPD 240

127 L-VARLADESGHYVLRWLPPPET-----PMTSHIREYVDVSAGNGAGSVORVELLEGRT 180

241 VHSRKGLEDDQLSVRWSPFPALKDFLFOAKYQIRIRVEDSV-----DKKVVDDVSNQIS 295

181 CVLSNLGRTRYTFVAVRARMAPSPFG-----GFWASMESEPSLLTP 221

296 CRLAGLKPGTVFVQVRCN----PFGYGSKKAGIWEWSHPTAATSP 339

RESULT 10 PRELIMINARY; PRT; 296 AA.

ID 018880 PRELIMINARY; PRT; 296 AA.

AC 018880; PRELIMINARY; PRT; 296 AA.

DT 01-JAN-1998 (TREMBLrel. 05, Created)

DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE PROLACTIN RECEPTOR SHORT FORM.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;

OC Bovidae; Bovinae; Bos.

OX NCB1_TaxID=9913;

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RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE-97375450; PubMed-9231767;
RA Schuler L.A., Nagel R.J., Gao J., Horseman N.D., Kessler M.A.;
RT "Prolactin receptor heterogeneity in bovine fetal and maternal
   tissues."
RL Endocrinology 138:3187-3194(1997).
DR EMBL: AF027403; AAB8399.1; -.
DR HSSP: P14787; IAN3.
DR InterPro: IPR002966; CRIA.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003528; Hematopo_receptor_L_F1.
DR Pfam: PF00041; fn3; 2.
DR SMART: SM00060; FN3; 2.
DR PROSITE: PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
KM Receptor.
SQ SEQUENCE 296 AA; 33854 MW; 9F1C15FB4IDE0787 CRC64;

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Query Match 13.3%; Score 159; DB 6; Length 296;
Best Local Similarity 24.6%; Pred No. 5.2e-07;
Matches 55; Conservative 36; Mismatches 103; Indels 30; Gaps 10;

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QY 16 ALIANGPPE---LLCTERLEDLVCFWEENASAGVPGNTSFSYQLEDEPKLCRLHQ 71
   :||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 20 SLINGSPPEKPKLVKCRSPGKETFCWMEPGADGL-PLNTYLLVHKGE---TLIHE 74
   :||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 72 APTARCAVFWCSLPTADTSSFPVLELRYTA-----ASGARVHVHINIEVLLDAV 125
   :||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 75 CDYKRTGGNSCYFSKRRHSIMKMVYITVAINQMGISSSDPLY---VHYTYIVEPEPPA 131
   :||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 126 GLVARL---ADESGHVYVLMPLPPETPMTHSH---IRYEDVNSAGNGAGSVORVEILEGRT 179
   :||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 132 NLTLKHEHEDKRPYIMIKMSPTMTDVKSGWFIIOYELRLRPEKATIDETHETLQ--T 189
   :||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 180 ECVLSNLRGRTRYTFAVRARMAEPSPGFWASAMSEPVSLTTPSD 223
   :||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 190 QLKIFNLPGOKYLVQIRCK---PDH-GYVSEWSPSSSIQIPND 229
   :||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

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RESULT 11
QJMS8 PRELIMINARY; PRT; 425 AA.
ID 09JMS8;
AC 09JMS8;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE CYTOKINE RECEPTOR LIKE MOLECULE 3 PRECURSOR.
GN CRLF1 OR CRLM3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RN SEQUENCE FROM N.A.
RA Hitoiyama T., Iwama A., Nakamura Y., Nakauchi H.;
RT "Cytokine receptor like molecule 3."
RL Submitted (Mar-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AB040038; BAA92777.1; -.
DR HSSP: P16471; IBP3.
DR MGD: MGI:1340030; Crlf1.
DR InterPro: IPR002996; CRIA.
DR InterPro: IPR003961; FN_III.
DR Pfam: PF00041; fn3; 2.
DR SMART: SM00060; FN3; 1.
KM Signal; Receptor.
ET SIGNAL 1 34
SQ SEQUENCE 425 AA; 46662 MW; 910535C629CA7056 CRC64;

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Query Match 13.2%; Score 157.5; DB 11; Length 425;
Best Local Similarity 25.9%; Pred. No. 1.1e-06;
Matches 59; Conservative 29; Mismatches 85; Indels 55; Gaps 13;

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QY 23 PERLLCTERLEDLVCFWEENASAGVPG-----NYSFYQLEDEPW---KLCRL 69
   :||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 141 PRNISCWSNMMDLTCRMT-----PGAHGETFLHTYSLTKYR--WYGQNTCEE 189
   :||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 70 HQAPTARGAVRFWCSLPTADTSSFPVLELRYTAAS--GAPRYH-RVYHINIEVLLDAPVG 126
   :||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 190 YHIVGPHS-----CHIP-KDALFPYELIWEATNTLSARSQDVLTLVDLVVTTDPPD 243
   :||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 127 L-VARLADESGHVYVLMPLPPET-----PYTHIREVDVNSAGNGAGSVORVEILEGRT 180
   :||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 244 VHVSRVGGLEDLVSRVWSPALKDPLFOAKYQIRYRVDVY-----DMKVVDVNSQTS 298
   :||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 181 CVLSNLRGRTRYTFAVRARMAEPSPG-----GFWASAMSEPVSLTTP 221
   :||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 299 CRLAGLPGTYVYFOVRCN-----PFGITYSKRAGLWSEWSHPTASTP 342
   :||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

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RESULT 12
ID 046561 PRELIMINARY; PRT; 581 AA.
AC 046561; P79205; 046574; 046573; P79203; 046569;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
DE PROLACTIN RECEPTOR PRECURSOR (PRL-R) (PRLR) (OPR).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_Taxid=9940;
RN [1]
RN SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE-MAMMARY GLAND, AND LIVER;
RX MEDLINE-98001468; PubMed-9343303;
RA Bignon C., Blinart N., Ormandy C., Schuler L.A., Kelly P.A., Djiane J.;
RT "Long and short forms of the ovine prolactin receptor: cDNA cloning
   and genomic analysis reveal that the two forms arise by different
   RT alternative splicing mechanisms in ruminants and in rodents."
RL J. Mol. Endocrinol. 19:109-120(1997).
RN [2]
RN SEQUENCE OF 61-395 FROM N.A., AND ALTERNATIVE SPLICING.
RC STRAIN-SCOTTISH BLACKFACE / ISOLANE M22/80; TISSUE-ANTERIOR PITUITARY;
RX MEDLINE-99049302; PubMed=9832462;
RA Tortorese D.J., Brooks J., Ingleton P.M., McNeill J.A.S.;
RT "Detection of prolactin receptor gene expression in the sheep
   RT pituitary gland and visualization of the specific translation of the
   RT signal in gonadotrophs."
RL Endocrinology 139:5215-5223(1998).
RN [3]
RN SEQUENCE OF 147-302 FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE-PERIL LIVER, AND CORPUS LUTEUM;
RA Anthony R.V., Smith G.W., Duong A., Pratt S.L., Smith M.F.;
RT "Two forms of the prolactin receptor messenger ribonucleic acid are
   RT present in ovine fetal liver and adult ovary."
RL Endocrine 3:291-295(1995).
RN [4]
RN FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
   PRLACTIN (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- ALTERNATIVE PRODUCTS: THREE ISOFORMS; LONG ISOFORM (L-OPR) (SHOWN
   CC HERE), SHORT ISOFORM (S-OPR) AND SOLUBLE ISOFORM; ARE PRODUCED BY
   CC ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED (LIVER,
   CC PITUITARY, ADRENAL GLAND, OVARY AND FETAL LIVER).
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC EMBL: AF041257; AAB96795.1; -.
CC EMBL: AF041977; AAB96920.1; -.
CC EMBL: AF041979; AAB97082.1; -.
CC EMBL: AF042358; AAB97744.1; -.
CC EMBL: AF042358; AAB97743.1; -.
CC EMBL: AF041978; AAB96965.1; -.
CC EMBL: Y10578; CAA71597.1; -.

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OY 145 PPETPMTS---HIREYDVASAGNG-----AGSVORVELLGRTECVLSNLRGTRRYTF 194
 DB 114 PTLVDYRSGMILTQYFIRIKPEKATEWETHFAGQOTQFKIL-----SLPGOKYLV 164
 OY 195 AVRAMAEPSPFGFWSAMSEPVSLTPSDL 224
 DB 165 QVRCK---PDH-GFWSEMSPESSIOIPNDV 190

RESULT 15

O9XS92 PRELIMINARY; PRT; 625 AA.
 AC O9XS92;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE PROLACTIN RECEPTOR PRECURSOR.
 GN PRL-R.
 OS Trichosurus vulpecula (Brush-tailed possum).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Metatheria; Diprotodontia; Phalangeridae; Trichosurus.
 OX NCBI_TaxID=9337;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=TESTIS;
 RX MEDLINE=99236966; PubMed=10221777;
 RA Demmer J.;
 RT "The prolactin receptor from the brushtail possum (Trichosurus
 vulpecula): cDNA cloning, expression and functional analysis.";
 RL Mol. Cell. Endocrinol. 148:119-127(1999).
 DR EMBL: AF098296; AAD27039.1; -
 DR HSSP: P14787; IAN3.
 DR InterPro: IPR002996; CRIA.
 DR InterPro: IPR003961; FN_TII.
 DR InterPro: IPR003528; Hematopo_receptor_L_F1.
 DR Pfam: PF00041; fn3; 2.
 DR SMART: SM00060; FN3; 1.
 DR PROSITE: PS01352; Hematopo_REC_L_F1; UNKNOWN_1.
 KW Signal; Receptor.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 625 PROLACTIN RECEPTOR.
 SQ SEQUENCE 625 AA; 70539 MW; 2097D72827C9DBB6 CRC64;

Query Match 11.6%; Score 139; DB 6; Length 625;
 Best Local Similarity 24.6%; Pred. No. 0.0001;
 Matches 56; Conservative 34; Mismatches 98; Indels 40; Gaps 11;

OY 9 PFESKAMLLARGPEELICFTEILEDVCFMEEASAGVPGNYSFSYQLEDEPWKLCR 68
 DB 31 FRIEK-----CRSPK-----ETFTCMWPKPSDGGI-PTNYTLFYRKEGE---SL 71
 OY 69 LHOAPTARGAVRFWCSLPTADTSSFPVPLRLRYTAAS-----GAPRYHVIHINEVYLD 122
 DB 72 THECPDYKTCGNSCYFNKKHHSIMVYLIWVNAITNOMGRMSSEPRY--VDVYIYVEPD 128
 OY 123 APVGL---VARLADSGHVVFLRWLPPETPMTS---HIREYDVASAGNGASVQRYEILE 176
 DB 129 PPLNTLEVKQPEDEKPYLMLKWSPPVLVDVRSGLTLQYELRLKPEKAA--EMETHFAG 186
 OY 177 GRTCEVLSNLRGTRRYTFVAVRAMAEPSPFGFWSAMSEPVSLTPSDL 224
 DB 187 QOTQKIFISLYLGQKYLVEVRCK---PDHG--WSQMSPESSITLIPSDI 230

Search completed: August 28, 2002, 17:40:15
 Job time: 546 sec

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